Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1. (Original) A method for the detection of cytosine methylation in DNA characterized in that the DNA to be investigated is brought into contact with a triplex-forming molecule which distinguishes between methylated and unmethylated DNA.

2. (Original) The method according to claim 1, further characterized in that the triplex-forming molecule forms a triplex with the DNA to be investigated, whereby triplex formation with unmethylated DNA is preferred over triplex formation with methylated DNA, and the triplex formation is used for the detection of the methylation status.

3. (Original) The method according to claim 1, further characterized in that oligonucleotides, peptide nucleic acid (PNA) oligomers, other oligonucleotide analogs or chimeras, or molecules derived from these classes of substance are used as the triplex-forming molecules.

4. (Currently amended) The method according to ~~one of claims~~ claim 1 ~~to 3~~, further characterized in that the triplex-forming molecule consists both a duplex-forming sequence as well as a triplex-forming sequence.

5. (Currently amended) The method according to ~~one of claims~~ claim 1 ~~to 4~~, further characterized in that the triplex-forming molecule comprises at least one modified nucleobase, which specifically or selectively binds to a cytosine in the triplex.

6. (Original) The method according to claim 5, further characterized in that N^4-substituted cytosine derivatives are used as nucleobases.

7. (Currently amended) The method according to ~~one of claims~~ claim 5 ~~to 6~~, further characterized in that N^4-(3-acetamidopropyl)cytosine or N^4-(6-amino-2-pyridinyl)cytosine is used as the nucleobase.

8. (Currently amended) The method according to ~~one of claims~~ claim 5 ~~to 7~~, further characterized in that N^4-substituted cytosines, which comprise additional modifications at position 3, are used as nucleobases.

9. (Original) The method according to claim 8, further characterized in that position 3 is modified with a methyl, ethyl or isopropyl group.

10. (Currently amended) The method according to ~~one of claims~~ claim 1 ~~to 9~~, further characterized in that the triplex-forming molecule bears a detectable label.

11. (Currently amended) The method according to ~~one of claims~~ claim 1 ~~to 10~~, further characterized in that the methylation status is detected via an *in-situ* hybridization.

12. (Currently amended) The method according to ~~one of claims~~ claim 1 ~~to 10~~, further characterized in that for the detection of the methylation status, the DNA is amplified, wherein due to the triplex formation, the amplification of methylated DNA is preferred over the amplification of unmethylated DNA.

13. (Currently amended) The method according to ~~one of claims~~ claim 1 ~~to 10~~, further characterized in that for the detection of the methylation status, the DNA is amplified, wherein due to the triplex formation, the amplification of unmethylated DNA is preferred over the amplification of methylated DNA.

14. (Currently amended) The method according to ~~one of claims~~ claim 12 ~~to 13~~, further characterized in that triplex-forming molecules are utilized, which also serve as primers in the amplification.

15. (Currently amended) The method according to ~~one of claims~~ claim 1 ~~to 12~~, further characterized in that structures which hinder amplification are formed by the triplex formation.

16. (Currently amended) The method according to ~~one of claims~~ claim 12 ~~to 15~~, further characterized in that deoxy-5-methylcytosine triphosphate, and not deoxycytosine triphosphate (dCTP), is utilized in the amplification.

17. (Currently amended) The method according to ~~one of claims~~ claim 12 ~~to 16~~, further characterized in that a real-time PCR is utilized for the amplification.

18. (Original) A method for the separation of methylated and unmethylated DNA characterized in that

(a) the DNA is brought into contact with a triplex-forming molecule,

(b) the triplex-forming molecule forms a triplex with the DNA, wherein triplex formation with unmethylated DNA is preferred over triplex formation with methylated DNA,

(c) the triplex formation is utilized for the separation.

19. (Original) A method for the specific introduction of DNA damage into unmethylated DNA, characterized in that

(a) the DNA is brought into contact with a triplex-forming molecule which bears a reactive chemical group,

(b) the triplex-forming molecule forms a triplex with the DNA, wherein triplex formation with unmethylated DNA is preferred over triplex formation with methylated DNA,

(c) the reactive chemical group is reacted with the DNA present in triplex form.

20. (Original) A method for the specific inhibition of replication of unmethylated DNA, characterized in that

(a) DNA is brought into contact with a triplex-forming molecule,

(b) the triplex-forming molecule forms a triplex with the DNA, wherein triplex formation with unmethylated DNA is preferred over triplex formation with methylated DNA,

(c) the replication of the DNA present in triplex form is inhibited.

21. (Original) A method for the specific inhibition of transcription of unmethylated DNA, characterized in that

(a) DNA is brought into contact with a triplex-forming molecule,

(b) the triplex-forming molecule forms a triplex with the DNA, wherein triplex formation with unmethylated DNA is preferred over triplex formation with methylated DNA,

(c) the transcription of the DNA present in triplex form is inhibited.

22. (Original) Use of oligonucleotides, peptide nucleic acid (PNA) oligomers, other oligonucleotide analogs or chimeras, or molecules derived from these substance classes, which contain N^4-(3-acetamidopropyl)cytosine, N^4-(6-amino-2-pyridinyl)cytosine or other N^4-substituted cytosine derivatives, for the therapy of disorders which are associated with cytosine demethylation.